

SEQUENCE LISTING

<110> Genox Research, Inc.

National Center for Child Health and Development

<120> Methods for examination for allergic diseases, and drugs for
treating allergic diseases

<130> G1-A0212-US

<140>

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<150> JP 2002-188490

<151> 2002-06-27

<160> 18

<170> PatentIn Ver. 2.0

<210> 1

<211> 3794

<212> DNA

<213> Homo sapiens

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<221> CDS

<222> (730).. (2607)

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caccgctcc ctactcgca cacacagaca caagcgcgca cacaggctcc gcacacacac 180

ttcgctctcc cgcgcgctca caccctctt gccctgagcc cttgccggtg cagcgcggcg 240

ccgcagctgg acgccccctcc cgggctcact ttgcaacgct gacggtgccg gcagtggccg 300

tggaggtggg aacagcggcg gcacctctcc ccctgggtcac agcccaagcc aggacgcccg 360

cggaaacctct cggctgtgct ctcccatgag tcgggatcgc agcatcccc accagccgct 420

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cctccagat atg ccc tgc gtc caa gcc caa tat agc cct tcc cct cca ggt 771

Met Pro Cys Val Gln Ala Gln Tyr Ser Pro Ser Pro Pro Gly

1

5

10

tcc agt tat gcg gcg cag aca tac agc tcg gaa tac acc acg gag atc 819

Ser Ser Tyr Ala Ala Gln Thr Tyr Ser Ser Glu Tyr Thr Thr Glu Ile

15

20

25

30

atg aac ccc gac tac acc aag ctg acc atg gac ctt ggc agc act gag 867

Met Asn Pro Asp Tyr Thr Lys Leu Thr Met Asp Leu Gly Ser Thr Glu

35

40

45

atc acg gct aca gcc acc acg tcc ctg ccc agc atc agt acc ttc gtg 915

Ile Thr Ala Thr Ala Thr Thr Ser Leu Pro Ser Ile Ser Thr Phe Val

50

55

60

gag ggc tac tcg agc aac tac gaa ctc aag cct tcc tgc gtg tac caa 963

Glu Gly Tyr Ser Ser Asn Tyr Glu Leu Lys Pro Ser Cys Val Tyr Gln

65	70	75	
atg cag cgg ccc ttg atc aaa gtg gag gag ggg cgg gcg ccc agc tac			1011
Met Gln Arg Pro Leu Ile Lys Val Glu Glu Gly Arg Ala Pro Ser Tyr			
80	85	90	
cat cac cat cac cac cac cac cac cac cac cac cat cac cag cag			1059
His His His His His His His His His His His His His His His Gln Gln			
95	100	105	110
cag cat cag cag cca tcc att cct cca gcc tcc agc ccg gag gac gag			1107
Gln His Gln Gln Pro Ser Ile Pro Pro Ala Ser Ser Pro Glu Asp Glu			
115	120	125	
gtg ctg ccc agc acc tcc atg tac ttc aag cag tcc cca ccg tcc acc			1155
Val Leu Pro Ser Thr Ser Met Tyr Phe Lys Gln Ser Pro Pro Ser Thr			
130	135	140	
ccc acc acg ccg gcc ttc ccc ccg cag gcg ggg gcg tta tgg gac gag			1203
Pro Thr Thr Pro Ala Phe Pro Pro Gln Ala Gly Ala Leu Trp Asp Glu			
145	150	155	
gca ctg ccc tcg gcg ccc ggc tgc atc gca ccc ggc ccg ctg ctg gac			1251
Ala Leu Pro Ser Ala Pro Gly Cys Ile Ala Pro Gly Pro Leu Leu Asp			
160	165	170	
ccg ccg atg aag gcg gtc ccc acg gtg gcc ggc gcg cgc ttc ccg ctc			1299
Pro Pro Met Lys Ala Val Pro Thr Val Ala Gly Ala Arg Phe Pro Leu			
175	180	185	190
ttc cac ttc aag ccc tcg ccg ccg cat ccc ccc gcg ccc agc ccg gcc			1347
Phe His Phe Lys Pro Ser Pro Pro His Pro Pro Ala Pro Ser Pro Ala			
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ggc ggc cac cac ctc ggc tac gac ccg acg gcc gct gcc gcg ctc agc			1395
Gly Gly His His Leu Gly Tyr Asp Pro Thr Ala Ala Ala Ala Leu Ser			

210	215	220	
ctg ccg ctg gga gcc gca gcc gcc gcg ggc agc cag gcc gcc gcg ctt			1443
Leu Pro Leu Gly Ala Ala Ala Ala Ala Gly Ser Gln Ala Ala Ala Leu			
225	230	235	
gag agc cac ccg tac ggg ctg ccg ctg gcc aag agg gcg gcc ccg ctg			1491
Glu Ser His Pro Tyr Gly Leu Pro Leu Ala Lys Arg Ala Ala Pro Leu			
240	245	250	
gcc ttc ccg cct ctc ggc ctc acg ccc tcc cct acc gcg tcc agc ctg			1539
Ala Phe Pro Pro Leu Gly Leu Thr Pro Ser Pro Thr Ala Ser Ser Leu			
255	260	265	270
ctg ggc gag agt ccc agc ctg ccg tgc ccg ccc agc agg agc tgc tgc			1587
Leu Gly Glu Ser Pro Ser Leu Pro Ser Pro Pro Ser Arg Ser Ser Ser			
275	280	285	
tct ggc gag ggc acg tgt gcc gtg tgc ggg gac aac gcc gcc tgc cag			1635
Ser Gly Glu Gly Thr Cys Ala Val Cys Gly Asp Asn Ala Ala Cys Gln			
290	295	300	
cac tac ggc gtg cga acc tgc gag ggc tgc aag ggc ttt ttc aag aga			1683
His Tyr Gly Val Arg Thr Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg			
305	310	315	
aca gtg cag aaa aat gca aaa tat gtt tgc ctg gca aat aaa aac tgc			1731
Thr Val Gln Lys Asn Ala Lys Tyr Val Cys Leu Ala Asn Lys Asn Cys			
320	325	330	
cca gta gac aag aga cgt cga aac cga tgt cag tac tgt cga ttt cag			1779
Pro Val Asp Lys Arg Arg Arg Asn Arg Cys Gln Tyr Cys Arg Phe Gln			
335	340	345	350
aag tgt ctc agt gtt gga atg gta aaa gaa gtt gtc cgt aca gat agt			1827
Lys Cys Leu Ser Val Gly Met Val Lys Glu Val Val Arg Thr Asp Ser			

355	360	365	
ctg aaa ggg agg aga ggt cgt ctg cct tcc aaa cca aag agc cca tta			1875
Leu Lys Gly Arg Arg Gly Arg Leu Pro Ser Lys Pro Lys Ser Pro Leu			
370	375	380	
caa cag gaa cct tct cag ccc tct cca cct tct cct cca atc tgc atg			1923
Gln Gln Glu Pro Ser Gln Pro Ser Pro Pro Ser Pro Pro Ile Cys Met			
385	390	395	
atg aat gcc ctt gtc cga gct tta aca gac tca aca ccc aga gat ctt			1971
Met Asn Ala Leu Val Arg Ala Leu Thr Asp Ser Thr Pro Arg Asp Leu			
400	405	410	
gat tat tcc aga tac tgt ccc act gac cag gct gct gca ggc aca gat			2019
Asp Tyr Ser Arg Tyr Cys Pro Thr Asp Gln Ala Ala Ala Gly Thr Asp			
415	420	425	430
gct gag cat gtg caa caa ttc tac aac ctc ctg aca gcc tcc att gat			2067
Ala Glu His Val Gln Gln Phe Tyr Asn Leu Leu Thr Ala Ser Ile Asp			
435	440	445	
gta tcc aga agc tgg gca gaa aag att ccg gga ttt act gat ctc ccc			2115
Val Ser Arg Ser Trp Ala Glu Lys Ile Pro Gly Phe Thr Asp Leu Pro			
450	455	460	
aaa gaa gat cag aca tta ctt att gaa tca gcc ttt ttg gag ctg ttt			2163
Lys Glu Asp Gln Thr Leu Leu Ile Glu Ser Ala Phe Leu Glu Leu Phe			
465	470	475	
gtc ctc aga ctt tcc atc agg tca aac act gct gaa gat aag ttt gtg			2211
Val Leu Arg Leu Ser Ile Arg Ser Asn Thr Ala Glu Asp Lys Phe Val			
480	485	490	
ttc tgc aat gga ctt gtc ctg cat cga ctt cag tgc ctt cgt gga ttt			2259
Phe Cys Asn Gly Leu Val Leu His Arg Leu Gln Cys Leu Arg Gly Phe			

495	500	505	510	
ggg gag tgg ctc gac tct att aaa gac ttt tcc tta aat ttg cag agc				2307
Gly Glu Trp Leu Asp Ser Ile Lys Asp Phe Ser Leu Asn Leu Gln Ser				
	515	520	525	
ctg aac ctt gat atc caa gcc tta gcc tgc ctg tca gca ctg agc atg				2355
Leu Asn Leu Asp Ile Gln Ala Leu Ala Cys Leu Ser Ala Leu Ser Met				
	530	535	540	
atc aca gaa aga cat ggg tta aaa gaa cca aag aga gtc gaa gag cta				2403
Ile Thr Glu Arg His Gly Leu Lys Glu Pro Lys Arg Val Glu Glu Leu				
	545	550	555	
tgc aac aag atc aca agc agt tta aaa gac cac cag agt aag gga cag				2451
Cys Asn Lys Ile Thr Ser Ser Leu Lys Asp His Gln Ser Lys Gly Gln				
	560	565	570	
gct ctg gag ccc acc gag tcc aag gtc ctg ggt gcc ctg gta gaa ctg				2499
Ala Leu Glu Pro Thr Glu Ser Lys Val Leu Gly Ala Leu Val Glu Leu				
	575	580	585	590
agg aag atc tgc acc ctg ggc ctc cag cgc atc ttc tac ctg aag ctg				2547
Arg Lys Ile Cys Thr Leu Gly Leu Gln Arg Ile Phe Tyr Leu Lys Leu				
	595	600	605	
gaa gac ttg gtg tct cca cct tcc atc att gac aag ctc ttc ctg gac				2595
Glu Asp Leu Val Ser Pro Pro Ser Ile Ile Asp Lys Leu Phe Leu Asp				
	610	615	620	
acc cta cct ttc taatcaggag cagtggagca gtgagctgcc tcctctccta				2647
Thr Leu Pro Phe				
	625			
gcacctgctt gctacgcagc aaagggatag gtttggaaac ctatcatttc ctgtccttcc				2707

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gaaggat

3794

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<212> PRT

<213> Homo sapiens

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Pro Asp Tyr Thr Lys Leu Thr Met Asp Leu Gly Ser Thr Glu Ile Thr
 35 40 45

Ala Thr Ala Thr Thr Ser Leu Pro Ser Ile Ser Thr Phe Val Glu Gly
 50 55 60

Tyr Ser Ser Asn Tyr Glu Leu Lys Pro Ser Cys Val Tyr Gln Met Gln
 65 70 75 80

Arg Pro Leu Ile Lys Val Glu Glu Gly Arg Ala Pro Ser Tyr His His
 85 90 95

His His His His His His His His His His His His Gln Gln Gln His
 100 105 110

Gln Gln Pro Ser Ile Pro Pro Ala Ser Ser Pro Glu Asp Glu Val Leu
 115 120 125

Pro Ser Thr Ser Met Tyr Phe Lys Gln Ser Pro Pro Ser Thr Pro Thr
 130 135 140

Thr Pro Ala Phe Pro Pro Gln Ala Gly Ala Leu Trp Asp Glu Ala Leu
145 150 155 160

Pro Ser Ala Pro Gly Cys Ile Ala Pro Gly Pro Leu Leu Asp Pro Pro
165 170 175

Met Lys Ala Val Pro Thr Val Ala Gly Ala Arg Phe Pro Leu Phe His
180 185 190

Phe Lys Pro Ser Pro Pro His Pro Pro Ala Pro Ser Pro Ala Gly Gly
195 200 205

His His Leu Gly Tyr Asp Pro Thr Ala Ala Ala Ala Leu Ser Leu Pro
210 215 220

Leu Gly Ala Ala Ala Ala Ala Gly Ser Gln Ala Ala Ala Leu Glu Ser
225 230 235 240

His Pro Tyr Gly Leu Pro Leu Ala Lys Arg Ala Ala Pro Leu Ala Phe
245 250 255

Pro Pro Leu Gly Leu Thr Pro Ser Pro Thr Ala Ser Ser Leu Leu Gly
260 265 270

Glu Ser Pro Ser Leu Pro Ser Pro Pro Ser Arg Ser Ser Ser Ser Gly
275 280 285

Glu Gly Thr Cys Ala Val Cys Gly Asp Asn Ala Ala Cys Gln His Tyr
290 295 300

Gly Val Arg Thr Cys Glu Gly Cys Lys Gly Phe Phe Lys Arg Thr Val
305 310 315 320

Gln Lys Asn Ala Lys Tyr Val Cys Leu Ala Asn Lys Asn Cys Pro Val
325 330 335

Asp Lys Arg Arg Arg Asn Arg Cys Gln Tyr Cys Arg Phe Gln Lys Cys
 340 345 350

Leu Ser Val Gly Met Val Lys Glu Val Val Arg Thr Asp Ser Leu Lys
 355 360 365

Gly Arg Arg Gly Arg Leu Pro Ser Lys Pro Lys Ser Pro Leu Gln Gln
 370 375 380

Glu Pro Ser Gln Pro Ser Pro Pro Ser Pro Pro Ile Cys Met Met Asn
 385 390 395 400

Ala Leu Val Arg Ala Leu Thr Asp Ser Thr Pro Arg Asp Leu Asp Tyr
 405 410 415

Ser Arg Tyr Cys Pro Thr Asp Gln Ala Ala Ala Gly Thr Asp Ala Glu
 420 425 430

His Val Gln Gln Phe Tyr Asn Leu Leu Thr Ala Ser Ile Asp Val Ser
 435 440 445

Arg Ser Trp Ala Glu Lys Ile Pro Gly Phe Thr Asp Leu Pro Lys Glu
 450 455 460

Asp Gln Thr Leu Leu Ile Glu Ser Ala Phe Leu Glu Leu Phe Val Leu
 465 470 475 480

Arg Leu Ser Ile Arg Ser Asn Thr Ala Glu Asp Lys Phe Val Phe Cys
 485 490 495

Asn Gly Leu Val Leu His Arg Leu Gln Cys Leu Arg Gly Phe Gly Glu
 500 505 510

Trp Leu Asp Ser Ile Lys Asp Phe Ser Leu Asn Leu Gln Ser Leu Asn
 515 520 525

Leu Asp Ile Gln Ala Leu Ala Cys Leu Ser Ala Leu Ser Met Ile Thr
 530 535 540

Glu Arg His Gly Leu Lys Glu Pro Lys Arg Val Glu Glu Leu Cys Asn
 545 550 555 560

Lys Ile Thr Ser Ser Leu Lys Asp His Gln Ser Lys Gly Gln Ala Leu
 565 570 575

Glu Pro Thr Glu Ser Lys Val Leu Gly Ala Leu Val Glu Leu Arg Lys
 580 585 590

Ile Cys Thr Leu Gly Leu Gln Arg Ile Phe Tyr Leu Lys Leu Glu Asp
 595 600 605

Leu Val Ser Pro Pro Ser Ile Ile Asp Lys Leu Phe Leu Asp Thr Leu
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Pro Phe
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<210> 3

<211> 17

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
 Synthesized Primer Sequence

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<210> 4

<211> 17

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

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gttttttttt ttttttc

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<210> 5

<211> 17

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

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<210> 6

<211> 10

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

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<210> 7
<211> 22
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Synthesized Primer Sequence

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<210> 8
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Synthesized Primer Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Probe Sequence

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<210> 10

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially —
Synthesized Primer Sequence

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<210> 11

<211> 25

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

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<210> 12

<211> 26

<212> DNA

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<400> 12

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<210> 13

<211> 23

<212> DNA

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<223> Description of Artificial Sequence:Artificially
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<210> 14

<211> 23

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

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<210> 15

<211> 2087

<212> DNA

<213> Homo sapiens

<400> 15

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<210> 16

<211> 19

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

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<210> 17

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<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Primer Sequence

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<210> 18

<211> 24

<212> DNA

<213> Artificial Sequence

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<223> Description of Artificial Sequence:Artificially
Synthesized Probe Sequence

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